1642

1600

#12

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/538,106

DATE: 02/11/2002

TIME: 09:17:02

Input Set : A:\HMV-38.02 sequence listing.txt
Output Set: N:\CRF3\02112002\I538106.raw

p.5

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 3 <110> APPLICANT: MCKEON, FRANK
 4         YANG, ANNIE
 5         LODA, MASSIMO
 6         SIGNORETTI, SABINA
 7         CRUM, CHRISTOPHER
 9 <120> TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
10         RELATED THERETO
12 <130> FILE REFERENCE: HMV-038.02
14 <140> CURRENT APPLICATION NUMBER: 09/538,106
15 <141> CURRENT FILING DATE: 2000-03-29
17 <150> PRIOR APPLICATION NUMBER: 09/174,493
18 <151> PRIOR FILING DATE: 1998-10-15
20 <150> PRIOR APPLICATION NUMBER: 60/087,216
21 <151> PRIOR FILING DATE: 1998-05-29
23 <150> PRIOR APPLICATION NUMBER: 60/062,076
24 <151> PRIOR FILING DATE: 1997-10-15
26 <160> NUMBER OF SEQ ID NOS: 53
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1926
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(1923)
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42   1               5                   10                  15
44 cag cat atc tgg gat ttt ctg gaa cag cct ata tgt tca gtt cag ccc      96
45 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
46           20                  25                  30
48 att gac ttg aac ttt gtg gat gaa cca tca gaa gat ggt gcg aca aac     144
49 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
50           35                  40                  45
52 aag att gag att agc atg gac tgt atc cgc atg cag gac tcg gac ctg     192
53 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
54       50                  55                  60
56 agt gac ccc atg tgg cca cag tac acg aac ctg ggg ctc ctg aac agc     240
57 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
58   65                  70                  75                  80
60 atg gac cag cag att cag aac ggc tcc tcg tcc acc agt ccc tat aac     288
61 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
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62                        85                    90                    95
64 aca gac cac gcg cag aac agc gtc acg gcg ccc tcg ccc tac gca cag    336
65 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
66             100                   105                   110
68 ccc agc tcc acc ttc gat gct ctc tct cca tca ccc gcc atc ccc tcc    384
69 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
70             115                   120                   125
72 aac acc gac tac cca ggc ccg cac agt ttc gac gtg tcc ttc cag cag    432
73 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
74        130                   135                   140
76 tcg agc acc gcc aag tcg gcc acc tgg acg tat tcc act gaa ctg aag    480
77 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
78 145                   150                   155                   160
80 aaa ctc tac tgc caa att gca aag aca tgc ccc atc cag atc aag gtg    528
81 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
82             165                   170                   175
84 atg acc cca cct cct cag gga gct gtt atc cgc gcc atg cct gtc tac    576
85 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
86             180                   185                   190
88 aaa aaa gct gag cac gtc acg gag gtg gtg aag cgg tgc ccc aac cat    624
89 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
90             195                   200                   205
92 gag ctg agc cgt gaa ttc aac gag gga cag att gcc cct cct agt cat    672
93 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
94        210                   215                   220
96 ttg att cga gta gag ggg aac agc cat gcc cag tat gta gaa gat ccc    720
97 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
98 225                   230                   235                   240
100 atc aca gga aga cag agt gtg ctg gta cct tat gag cca ccc cag gtt    768
101 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
102                   245                   250                   255
104 ggc act gaa ttc acg aca gtc ttg tac aat ttc atg tgt aac agc agt    816
105 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
106             260                   265                   270
108 tgt gtt gga ggg atg aac cgc cgt cca att tta atc att gtt act ctg    864
109 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
110             275                   280                   285
112 gaa acc aga gat ggg caa gtc ctg ggc cga cgc tgc ttt gag gcc cgg    912
113 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
114        290                   295                   300
116 atc tgt gct tgc cca gga aga gac agg aag gcg gat gaa gat agc atc    960
117 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
118 305                   310                   315                   320
120 aga aag cag caa gtt tcg gac agt aca aag aac ggt gat ggt acg aag    1008
121 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
122                   325                   330                   335
124 cgc ccg ttt cgt cag aac aca cat ggt atc cag atg aca tcc atc aag    1056
125 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
126             340                   345                   350
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128 aaa cga aga tcc cca gat gat gaa ctg tta tac tta cca gtg agg ggc    1104
129 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
130         355                 360                 365
132 cgt gag act tat gaa atg ctg ttg aag atc aaa gag tcc ctg gaa ctc    1152
133 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
134     370                 375                 380
136 atg cag tac ctt cct cag cac aca att gaa acg tac agg caa cag caa    1200
137 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
138 385                 390                 395                 400
140 cag cag cag cac cag cac tta ctt cag aaa cag acc tca ata cag tct    1248
141 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
142             405                 410                 415
144 cca tct tca tat ggt aac agc tcc cca cct ctg aac aaa atg aac agc    1296
145 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
146             420                 425                 430
148 atg aac aag ctg cct tct gtg agc cag ctt atc aac cct cag cag cgc    1344
149 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
150         435                 440                 445
152 aac gcc ctc act cct aca acc att cct gat ggc atg gga gcc aac att    1392
153 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
154     450                 455                 460
156 ccc atg atg ggc acc cac atg cca atg gct gga gac atg aat gga ctc    1440
157 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
158 465                 470                 475                 480
160 agc ccc acc cag gca ctc cct ccc cca ctc tcc atg cca tcc acc tcc    1488
161 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
162             485                 490                 495
164 cac tgc aca ccc cca cct ccg tat ccc aca gat tgc agc att gtc agt    1536
165 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
166             500                 505                 510
168 ttc tta gcg agg ttg ggc tgt tca tca tgt ctg gac tat ttc acg acc    1584
169 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
170         515                 520                 525
172 cag ggg ctg acc acc atc tat cag att gag cat tac tcc atg gat gat    1632
173 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
174     530                 535                 540
176 ctg gca agt ctg aaa atc cct gag caa ttt cga cat gcg atc tgg aag    1680
177 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
178 545                 550                 555                 560
180 ggc atc ctg gac cac cgg cag ctc cac gaa ttc tcc tcc cct tct cat    1728
181 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
182             565                 570                 575
184 ctc ctg cgg acc cca agc agt gcc tct aca gtc agt gtg ggc tcc agt    1776
185 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
186             580                 585                 590
188 gag acc cgg ggt gag cgt gtt att gat gct gtg cga ttc acc ctc cgc    1824
189 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
190         595                 600                 605
192 cag acc atc tct ttc cca ccc cga gat gag tgg aat gac ttc aac ttt    1872
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RAW SEQUENCE LISTING   DATE: 02/11/2002
PATENT APPLICATION: US/09/538,106   TIME: 09:17:02

Input Set : A:\HMV-38.02 sequence listing.txt
Output Set: N:\CRF3\02112002\I538106.raw

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193 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
194     610             615             620
196 gac atg gat gct cgc cgc aat aag caa cag cgc atc aaa gag gag ggg      1920
197 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
198 625             630             635             640
200 gag tga                                                             1926
201 Glu
204 <210> SEQ ID NO: 2
205 <211> LENGTH: 1551
206 <212> TYPE: DNA
207 <213> ORGANISM: Homo sapiens
209 <220> FEATURE:
210 <221> NAME/KEY: CDS
211 <222> LOCATION: (1)..(1548)
213 <400> SEQUENCE: 2
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216  1               5                   10                  15
218 cag cat atc tgg gat ttt ctg gaa cag cct ata tgt tca gtt cag ccc      96
219 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
220             20                  25                  30
222 att gac ttg aac ttt gtg gat gaa cca tca gaa gat ggt gcg aca aac      144
223 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
224             35                  40                  45
226 aag att gag att agc atg gac tgt atc cgc atg cag gac tcg gac ctg      192
227 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
228     50                  55                  60
230 agt gac ccc atg tgg cca cag tac acg aac ctg ggg ctc ctg aac agc      240
231 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
232 65                  70                  75                  80
234 atg gac cag cag att cag aac ggc tcc tcg tcc acc agt ccc tat aac      288
235 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
236             85                  90                  95
238 aca gac cac gcg cag aac agc gtc acg gcg ccc tcg ccc tac gca cag      336
239 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
240             100                 105                 110
242 ccc agc tcc acc ttc gat gct ctc tct cca tca ccc gcc atc ccc tcc      384
243 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
244         115                 120                 125
246 aac acc gac tac cca ggc ccg cac agt ttc gac gtg tcc ttc cag cag      432
247 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
248     130                 135                 140
250 tcg agc acc gcc aag tcg gcc acc tgg acg tat tcc act gaa ctg aag      480
251 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
252 145                 150                 155                 160
254 aaa ctc tac tgc caa att gca aag aca tgc ccc atc cag atc aag gtg      528
255 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
256             165                 170                 175
258 atg acc cca cct cct cag gga gct gtt atc cgc gcc atg cct gtc tac      576
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259 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
260             180                 185                 190
262 aaa aaa gct gag cac gtc acg gag gtg gtg aag cgg tgc ccc aac cat    624
263 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
264         195                 200                 205
266 gag ctg agc cgt gaa ttc aac gag gga cag att gcc cct cct agt cat    672
267 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
268         210                 215                 220
270 ttg att cga gta gag ggg aac agc cat gcc cag tat gta gaa gat ccc    720
271 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
272 225                 230                 235                 240
274 atc aca gga aga cag agt gtg ctg gta cct tat gag cca ccc cag gtt    768
275 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
276                 245                 250                 255
278 ggc act gaa ttc acg aca gtc ttg tac aat ttc atg tgt aac agc agt    816
279 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
280             260                 265                 270
282 tgt gtt gga ggg atg aac cgc cgt cca att tta atc att gtt act ctg    864
283 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
284         275                 280                 285
286 gaa acc aga gat ggg caa gtc ctg ggc cga cgc tgc ttt gag gcc cgg    912
287 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
288     290                 295                 300
290 atc tgt gct tgc cca gga aga gac agg aag gcg gat gaa gat agc atc    960
291 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
292 305                 310                 315                 320
294 aga aag cag caa gtt tcg gac agt aca aag aac ggt gat ggt acg aag   1008
295 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
296                 325                 330                 335
298 cgc ccg ttt cgt cag aac aca cat ggt atc cag atg aca tcc atc aag   1056
299 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
300             340                 345                 350
302 aaa cga aga tcc cca gat gat gaa ctg tta tac tta cca gtg agg ggc   1104
303 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
304         355                 360                 365
306 cgt gag act tat gaa atg ctg ttg aag atc aaa gag tcc ctg gaa ctc   1152
307 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
308     370                 375                 380
310 atg cag tac ctt cct cag cac aca att gaa acg tac agg caa cag caa   1200
311 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
312 385                 390                 395                 400
314 cag cag cag cac cag cac tta ctt cag aaa cag acc tca ata cag tct   1248
315 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
316             405                 410                 415
318 cca tct tca tat ggt aac agc tcc cca cct ctg aac aaa atg aac agc   1296
319 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
320             420                 425                 430
322 atg aac aag ctg cct tct gtg agc cag ctt atc aac cct cag cag cgc   1344
323 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <225> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 02/11/2002
PATENT APPLICATION: US/09/538,106   TIME: 09:17:03

Input Set : **A:\HMV-38.02 sequence listing.txt**
Output Set: **N:\CRF3\02112002\I538106.raw**

L:3189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27